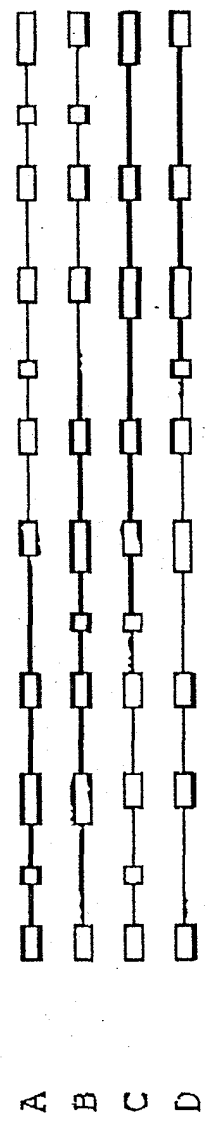


00000 00000000

Fig. 1



09747410-40000

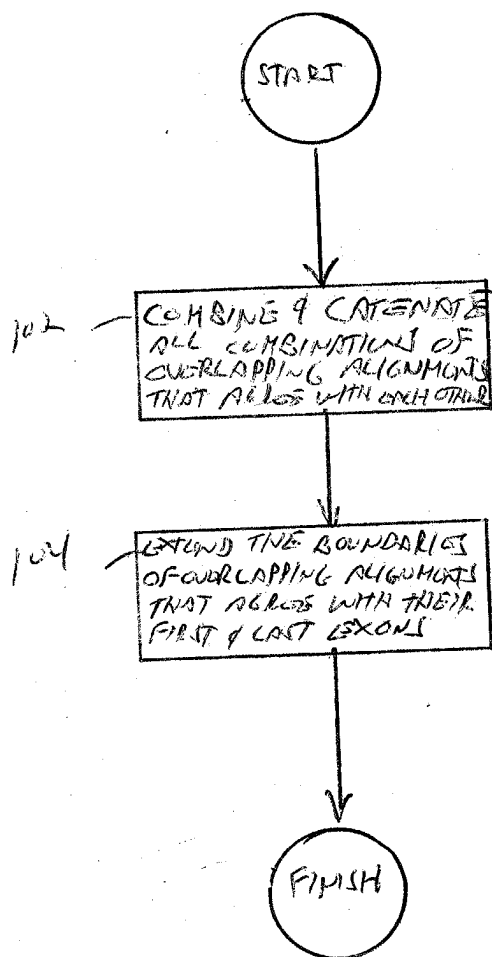
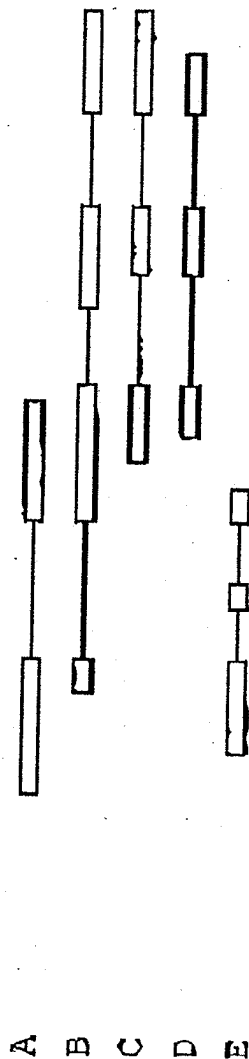
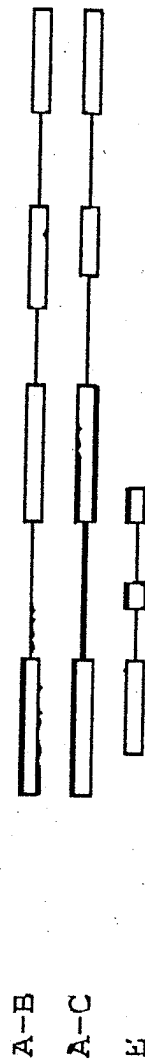


Fig. 2

Fig. 3  
Input:



After Step 1:



After Step 2:

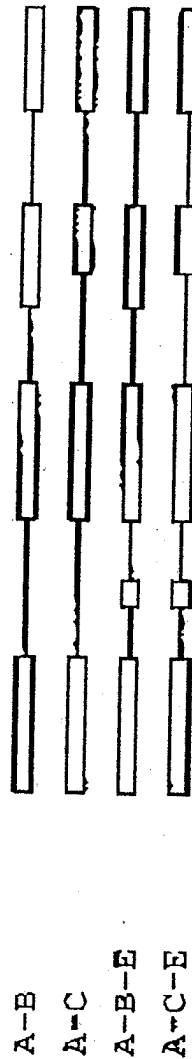
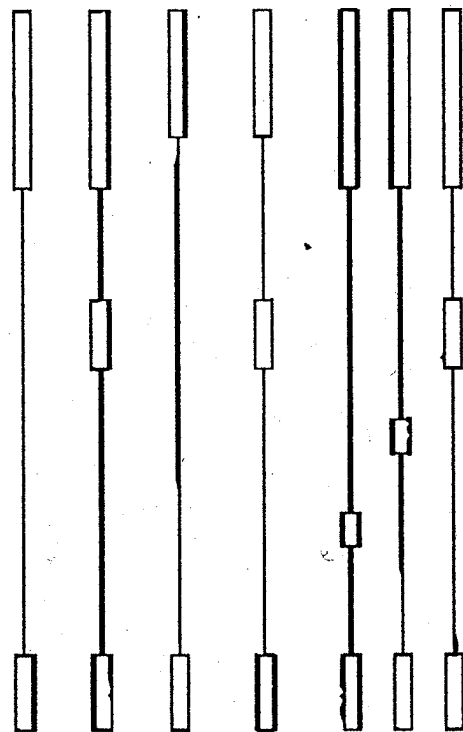


Fig. 4

- 40 - "Normal" gene splicing
- 41 - Cassette Exon
- 42 - Shifted splice site
- 43 - Cassette Exon w/ shift
- 44 - Variable exons



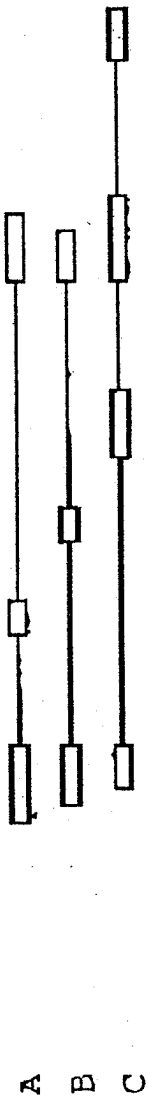
[illegible]

The diagram shows four horizontal bars representing different recombination events. Each bar is divided into segments of varying lengths and positions, indicating the relative positions of genes A, B, and C. The labels A, A-B, A-C, and A-B-C are positioned below their respective bars.

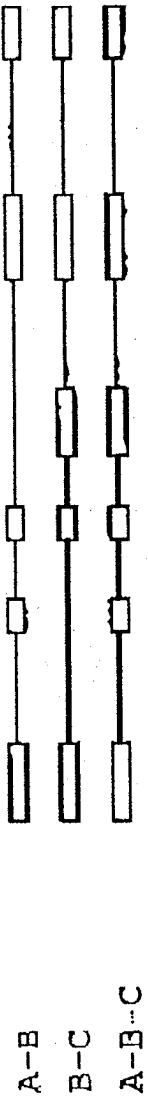
- A**: A single long bar with a small segment at the left end.
- A-B**: A bar with a small segment at the left end and a small segment in the middle.
- A-C**: A bar with a small segment at the left end and a small segment at the right end.
- A-B-C**: A bar with a small segment at the left end, a small segment in the middle, and a small segment at the right end.

Fig. 6

Input:



After Combining (3 examples):



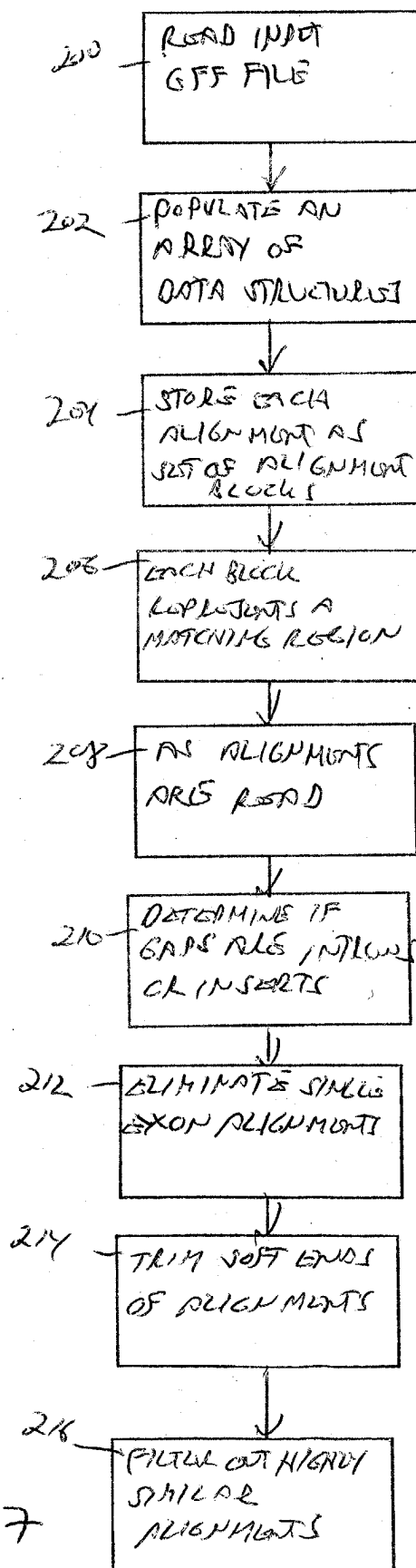
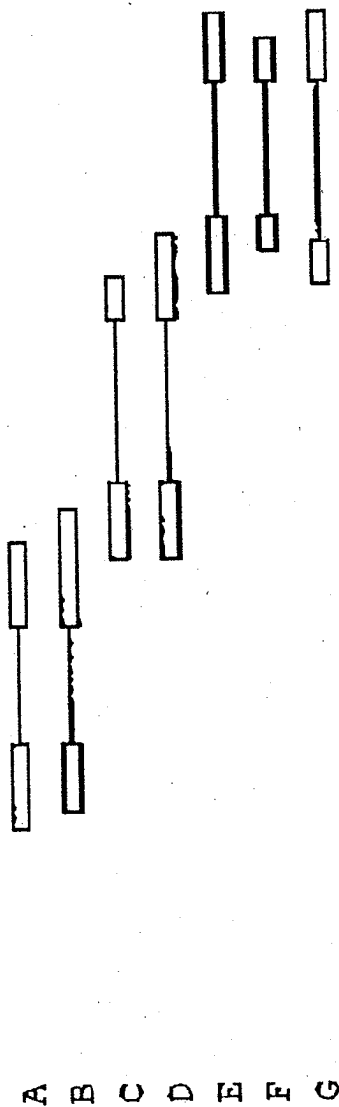


Fig. 7

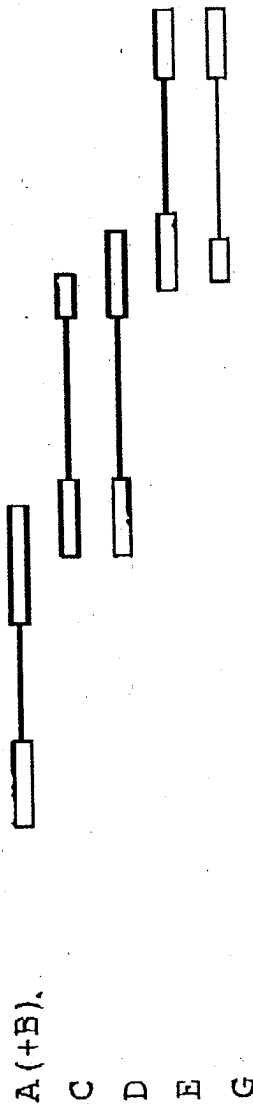
Fig. 8

Input:

00000101111100



After Filtering:



After Merging:





102

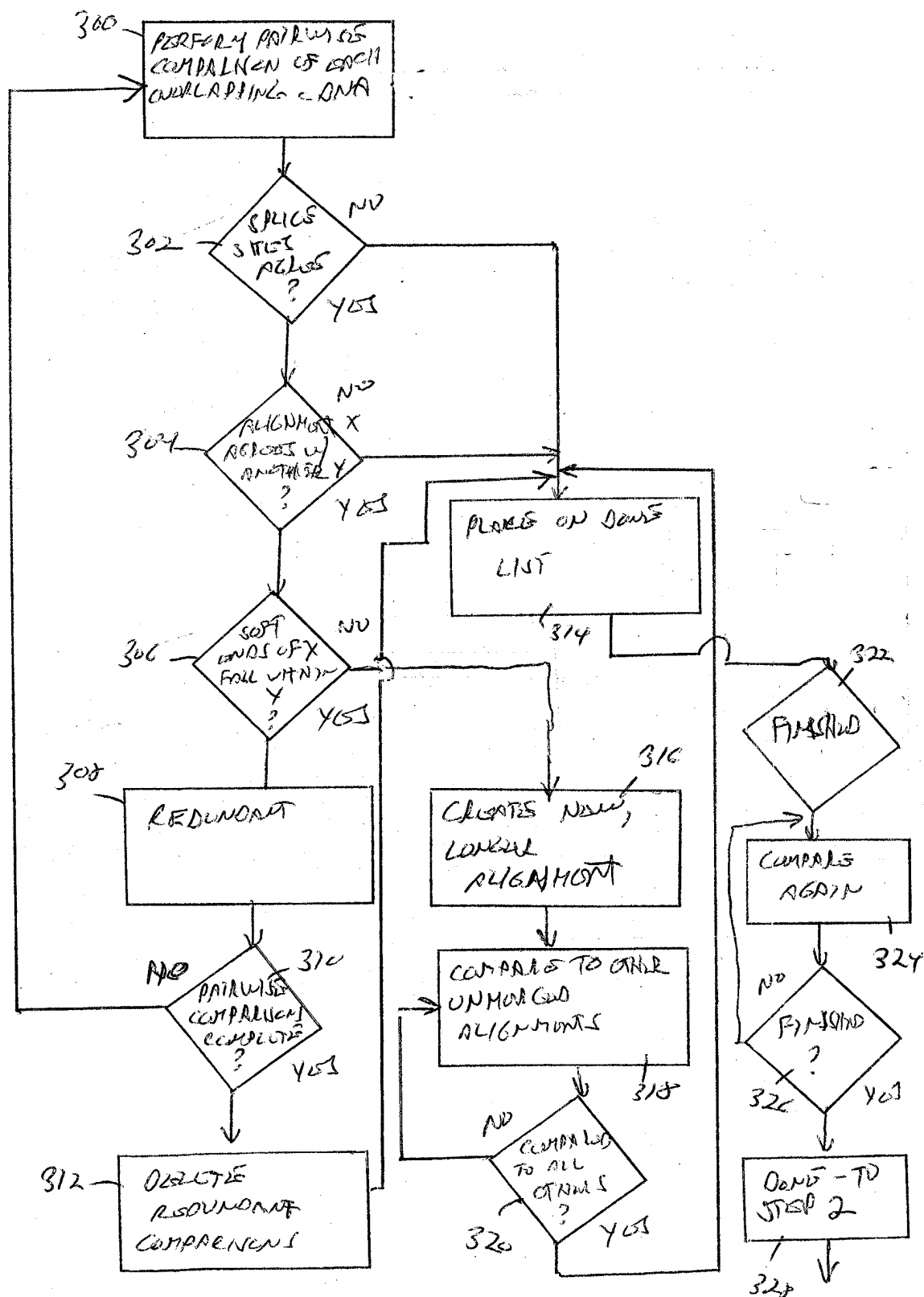
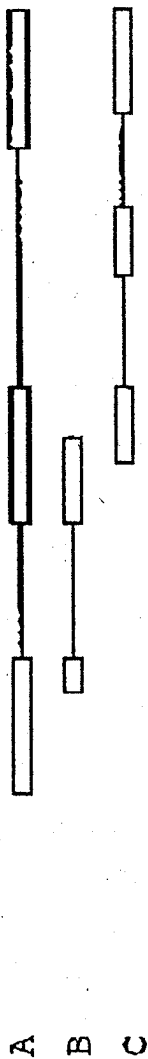


Fig 9

Fig. 10

Input:



Results if alignment B is discarded early:



Results if alignment B is discarded later:

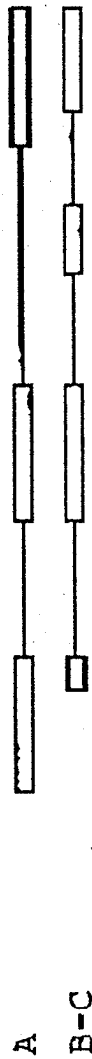
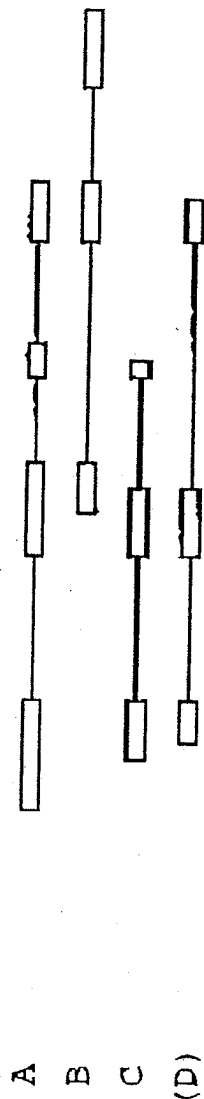




Fig. 12

After Merging:



After Extending:

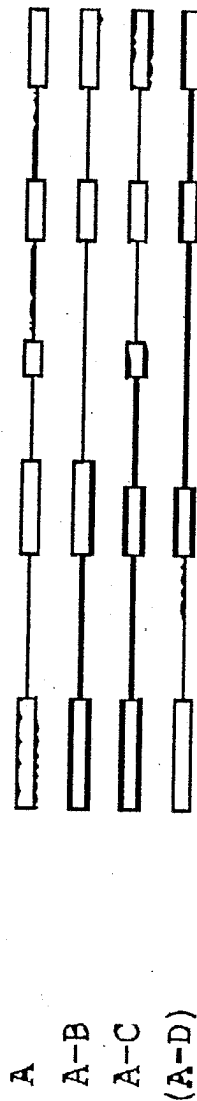


Fig. 13

[illegible]